

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2619	100.0	514	7	ADG63312	Adg63312 Human IMP
2	2609	99.6	514	7	ADG63349	Adg63349 Human IMP
3	2605	99.5	514	2	AAR05432	Aar05432 Human IMP
4	2605	99.5	514	5	AAE18189	Aae18189 Human wil
5	2605	99.5	514	7	ADG63310	Adg63310 Human wil
6	2605	99.5	514	7	ADJ68634	Adj68634 Human hea
7	2605	99.5	514	8	ADO19228	Ado19228 Human PRO
8	2605	99.5	529	8	ADR66377	Adr66377 Human pro
9	2605	99.5	529	8	ADR66719	Adr66719 Human pro
10	2601	99.3	514	7	ADG63316	Adg63316 Human IMP
11	2601	99.3	514	7	ADG63314	Adg63314 Human IMP
12	2597	99.2	514	7	ADG63318	Adg63318 Human IMP
13	2595	99.1	514	5	AAU10695	Aau10695 Reference
14	2595	99.1	514	5	AAE18186	Aae18186 Human wil
15	2595	99.1	514	8	ADS88152	Ads88152 Human pro
16	2590	98.9	514	7	ADG63320	Adg63320 Human IMP
17	2569	98.1	514	7	ADG63340	Adg63340 Mouse IMP
18	2559	97.7	514	2	AAR05431	Aar05431 Chinese h
19	2555	97.6	514	7	ADG63338	Adg63338 Mouse wil
20	2234	85.3	514	5	AAE18188	Aae18188 Human wil
21	2234	85.3	514	5	ADI17228	Adi17228 Human NOV
22	2234	85.3	563	6	ADA54125	Ada54125 Human pro
23	2229	85.1	514	5	AAE18257	Aae18257 Human typ

RESULT 3  
AAR05432  
ID AAR05432 standard; protein; 514 AA.  
XX  
AC AAR05432;  
XX  
DT 25-MAR-2003 (revised)  
DT 31-AUG-1990 (first entry)  
XX  
DE Human IMPDH.  
XX  
KW Inosine 5'-mono-phosphate dehydrogenase; hepatomas;  
KW guanosine monophosphate.  
XX  
OS Homo sapiens.  
XX  
PN WO9001545-A.  
XX  
PD 22-FEB-1990.  
XX  
PF 02-AUG-1989; 89WO-US003344.  
XX  
PR 12-AUG-1988; 88US-00232302.  
XX  
PA (ARCH-) ARCH DEV CORP.  
XX  
PI Collart FR, Huberman E;  
XX  
DR WPI; 1990-083504/11.  
DR P-PSDB; AAR05432.  
XX  
PT DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase - used to  
PT detect high levels of enzyme indicative of tumour cells, esp. hepatomas,  
PT and to produce guanosine mono-phosphate.  
XX  
PS Claim 8; Fig 1; 51pp; English.  
XX  
CC A 35 aa segment corresponds to deduced aa residues 336-370 in both the  
CC human and Chinese hamster proteins. See also AAQ03541. (Updated on 25-MAR  
CC -2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 514 AA;  
  
Query Match 99.5%; Score 2605; DB 2; Length 514;  
Best Local Similarity 99.6%; Pred. No. 7.9e-246;  
Matches 512; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 MADYLI SGGTSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQV DLTSA LTKKIT 60  
Db 1 MADYLI SGGTSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQV DLTSA LTKKIT 60  
  
Qy 61 LKTPLVSSPM DTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQGFITDPVV 120  
Db 61 LKTPLVSSPM DTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQGFITDPVV 120  
  
Qy 121 LSPKDRV RDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDFLKEEEHDCFLEEIMT 180  
Db 121 LSPKDRV RDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDFLKEEEHDCFLEEIMT 180

Db 121 LSPKDRVRDVFEAKRHGFCGIPITDTGRMGSRLVGISSRDIDFLKEEEHDCFLEEIMT 180  
Qy 181 KREDLVVAAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 181 KREDLVVAAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240  
Qy 241 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVLDSSQGNSIFQINMIKYIKDKYPNLQVI 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 241 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVLDSSQGNSIFQINMIKYIKDKYPNLQVI 300  
Qy 301 GGNVVTAAQAKNLIDAGVDALRVMGSGSICIQEVLACGRPQATAVYKVYEYARRFGVP 360  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 301 GGNVVTAAQAKNLIDAGVDALRVMGSGSICITQEVLACGRPQATAVYKVSEYARRFGVP 360  
Qy 361 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKRYRGMGSLDAM 420  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 361 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKRYRGMGSLDAM 420  
Qy 421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPLIAGIQHSCQDIGAKSLTQVR 480  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPLIAGIQHSCQDIGAKSLTQVR 480  
Qy 481 AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF 514  
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Db 481 AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF 514

Database : Published\_Applications\_AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

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12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB ID	
<hr/>						
1	2619	100.0	514	10	US-09-846-637A-4	Sequence 4, Appl
2	2605	99.5	514	9	US-09-853-918-63	Sequence 63, Appl
3	2605	99.5	514	10	US-09-846-637A-2	Sequence 2, Appl
4	2605	99.5	514	16	US-10-408-765A-440	Sequence 440, App
5	2601	99.3	514	10	US-09-846-637A-6	Sequence 6, Appl
6	2601	99.3	514	10	US-09-846-637A-8	Sequence 8, Appl
7	2597	99.2	514	10	US-09-846-637A-10	Sequence 10, Appl
8	2595	99.1	514	9	US-09-853-918-49	Sequence 49, Appl
9	2590	98.9	514	10	US-09-846-637A-12	Sequence 12, Appl

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	2605	99.5	514	3	US-08-925-230-7	Sequence 7, Appli
2	2605	99.5	514	4	US-09-712-372-7	Sequence 7, Appli
3	2595	99.1	514	4	US-09-538-092-913	Sequence 913, App
4	2595	99.1	607	4	US-09-949-016-11614	Sequence 11614, A
5	2559	97.7	514	3	US-08-925-230-8	Sequence 8, Appli
6	2559	97.7	514	4	US-09-712-372-8	Sequence 8, Appli
7	2222	84.8	514	4	US-09-538-092-973	Sequence 973, App
8	1607.5	61.4	523	4	US-09-538-092-584	Sequence 584, App
9	1210.5	46.2	371	3	US-09-212-247C-9	Sequence 9, Appli
10	906	34.6	510	4	US-09-134-000C-5141	Sequence 5141, Ap
11	885	33.8	495	4	US-09-107-532A-4081	Sequence 4081, Ap
12	865	33.0	488	4	US-09-710-279-2308	Sequence 2308, Ap
13	865	33.0	494	3	US-09-134-001C-5024	Sequence 5024, Ap
14	862.5	32.9	558	4	US-09-252-991A-18187	Sequence 18187, A
15	859.5	32.8	497	4	US-09-328-352-6297	Sequence 6297, Ap
16	819	31.3	510	4	US-09-489-039A-11778	Sequence 11778, A
17	816	31.2	487	4	US-09-809-665A-169	Sequence 169, App
18	811	31.0	487	4	US-09-809-665A-24	Sequence 24, Appli
19	807.5	30.8	492	4	US-09-583-110-4390	Sequence 4390, Ap

RESULT 1  
US-08-925-230-7  
; Sequence 7, Application US/08925230  
; Patent No. 6147194  
; GENERAL INFORMATION:  
; APPLICANT: Collart, Frank  
; APPLICANT: Huberman, Eliezer  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH  
; TITLE OF INVENTION: AND GMP PRODUCTION  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/925,230  
; FILING DATE: September 8, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 5,665,583  
; FILING DATE: 12-AUG-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: ARCD:274  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 514 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-925-230-7  
  
Query Match 99.5%; Score 2605; DB 3; Length 514;  
Best Local Similarity 99.6%; Pred. No. 4.2e-250;  
Matches 512; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 MADYLI SGGTSY VPDDGLTA QQ LFNC GDGL TYND FLI LPGY IDFT ADQV DLTS AL TKIT 60  
Db 1 MADYLI SGGTSY VPDDGLTA QQ LFNC GDGL TYND FLI LPGY IDFT ADQV DLTS AL TKIT 60  
  
Qy 61 LKTPLVSSPMDTVTEAGMA IAMALTGGIGFI HHNCTPEFQANE VRKVKKY EQGFITDPVV 120  
Db 61 LKTPLVSSPMDTVTEAGMA IAMALTGGIGFI HHNCTPEFQANE VRKVKKY EQGFITDPVV 120  
  
Qy 121 LSPKDRVRDVFEAKARHGFCGI PITDTGRMGSRLVGI ISSRDIDFLKEEEHDCFLEEIMT 180

Db ||||||| 121 LSPKDRVDRVFEAKRGFCGIPITDTGRMGSRLVGISSRDIDFLKEEHDCFLEEIMT 180

Qy 181 KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240

Db ||||||| 181 KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240

Qy 241 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVLDSSEQNSIFQINMIKYIKDKYPNLQVI 300

Db ||||||| 241 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVLDSSEQNSIFQINMIKYIKDKYPNLQVI 300

Qy 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICIQEVLACRPQATAVYKVYEYARRFGVP 360

Db ||||||| 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLACRPQATAVYKVSEYARRFGVP 360

Qy 361 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420

Db ||||||| 361 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420

Qy 421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPLIAGIQHSCQDIGAKSLTQVR 480

Db ||||||| 421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPLIAGIQHSCQDIGAKSLTQVR 480

Qy 481 AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF 514

Db ||||||| 481 AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF 514

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

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SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	ID
1	2595	99.1	514	1	A31997	IMP dehydrogenase
2	2559	97.7	514	1	B31997	IMP dehydrogenase
3	2555	97.6	514	1	JT0565	IMP dehydrogenase
4	2222	84.8	514	1	A35566	IMP dehydrogenase
5	1764.5	67.4	537	1	S41064	IMP dehydrogenase
6	1635.5	62.4	537	1	S59508	IMP dehydrogenase
7	1610.5	61.5	524	1	S50890	IMP dehydrogenase
8	1607.5	61.4	523	1	S59402	IMP dehydrogenase
9	1589.5	60.7	523	1	S48997	IMP dehydrogenase
10	1473.5	56.3	524	1	T40127	IMP dehydrogenase
11	1385.5	52.9	512	1	A55407	IMP dehydrogenase
12	1363.5	52.1	514	1	A38668	IMP dehydrogenase
13	1324.5	50.6	499	1	T32709	IMP dehydrogenase
14	1155	44.1	502	2	F86298	IMP dehydrogenase
15	1106.5	42.2	503	1	JC4999	IMP dehydrogenase
16	1043.5	39.8	403	2	S53477	IMP dehydrogenase
17	966.5	36.9	485	2	G81308	IMP dehydrogenase
18	958	36.6	485	2	D97232	IMP dehydrogenase

RESULT 1

A31997

IMP dehydrogenase (EC 1.1.1.205) II - human

N;Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH) type II

C;Species: Homo sapiens (man)

C;Date: 21-May-1990 #sequence\_revision 22-May-1998 #text\_change 09-Jul-2004

C;Accession: I52303; I54184; A92676; B35566; A31997; A94550

R;Glesne, D.A.; Huberman, E.

Biochem. Biophys. Res. Commun. 205, 537-544, 1994

A;Title: Cloning and sequence of the human type II IMP dehydrogenase gene.

A;Reference number: I52303; MUID:95091778; PMID:7999076

A;Accession: I52303

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-514 <GLE1>

A;Cross-references: UNIPROT:P12268; GB:L33842; NID:g602457; PIDN:AAA67054.1;

PID:g602458

R;Glesne, D.A.; Collart, F.R.; Varkony, T.; Drabkin, H.; Huberman, E.

Genomics 16, 274-277, 1993

A;Title: Chromosomal localization and structure of the human type II IMP dehydrogenase gene.

A;Reference number: I54184; MUID:93252398; PMID:8098009

A;Accession: I54184

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 461-514 <GLE2>

A;Cross-references: GB:L08114; NID:g292239; PIDN:AAA36113.1; PID:g292240

R;Collart, F.R.; Huberman, E.

J. Biol. Chem. 263, 15769-15772, 1988

A;Title: Cloning and sequence analysis of the human and Chinese hamster inosine-5'-monophosphate dehydrogenase cDNAs.

A;Reference number: A92676; MUID:89008491; PMID:2902093

A;Accession: A92676

A;Molecule type: mRNA

A;Residues: 1-189, 'RS', 192-514 <COL>

A;Cross-references: GB:J04208; NID:g186391; PIDN:AAA36112.1; PID:g307066

A;Note: submitted to the Protein Sequence Database, November 1989

R;Natsumeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.

J. Biol. Chem. 265, 5292-5295, 1990

A;Title: Two distinct cDNAs for human IMP dehydrogenase.

A;Reference number: A35566; MUID:90203022; PMID:1969416

A;Accession: B35566

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-514 <NAT>

C;Comment: mRNA for IMP dehydrogenase I (see PIR:A35566) predominated in normal leukocytes, whereas that for IMP dehydrogenase II predominated in ovarian tumor cells.

C;Genetics:

A;Gene: GDB:IMPDH2

A;Cross-references: GDB:128086; OMIM:146691

A;Map position: 3p24.2-3p21.2

A;Introns: 33/2; 49/3; 83/3; 108/3; 177/3; 207/1; 274/1; 304/1; 336/1; 432/2; 480/2; 508/2

C;Function:

A;Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of water to xanthosine 5'-phosphate  
A;Pathway: purine nucleotide biosynthesis  
C;Superfamily: inosine-5'-monophosphate dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology; IMP dehydrogenase catalytic homology  
C;Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis  
F;30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>  
F;117-168/Domain: CBS homology <CBS1>  
F;184-232/Domain: CBS homology <CBS2>  
F;233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>  
F;331/Active site: Cys #status predicted

Query Match 99.1%; Score 2595; DB 1; Length 514;  
Best Local Similarity 99.2%; Pred. No. 8.7e-159;  
Matches 510; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MADYLI SGGSYV PDDGLTAQQLFNC GDGLTY NDFLILPGYIDFTADQV DLTSA LTKIT 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
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Qy 61 LKTPLVSS PMDTVTEAGMA IAMALTGGIGFI HHNCTPEFQANEVRKVKKYEQGFI TDPVV 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 61 LKTPLVSS PMDTVTEAGMA IAMALTGGIGFI HHNCTPEFQANEVRKVKKYEQGFI TDPVV 120  
  
Qy 121 LSPKDRV RDVFEAKARHGFCGIPITDTGRM GSRLVGI ISSRDIDFLKEE HDCFLEEIMT 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 121 LSPKDRV RDVFEAKARHGFCGIPITDTGRM GSRLVGI ISSRDIDFLKEE HDCFLEEIMT 180  
  
Qy 181 KREDLV VAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240  
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Db 181 KREDLV VAPAGITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA 240  
  
Qy 241 KKQLLCGAAIGTHE DDKYRL DLLAQAGV D VVLDSSQGNSIFQINMI KYIKDKY PNLQVI 300  
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Db 241 KKQLLCGAAIGTHE DDKYRL DLLAQAGV D VVLDSSQGNSIFQINMI KYIKDKY PNLQVI 300  
  
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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 301 GGNVVTAAQAKNLIDAGV D ALRVGM GS SICITQEV LACGRP QATA VYKV SEYARRFGVP 360  
  
Qy 361 VIADGGI QNVGHI AKALALGASTVMMG SLLAATTEAPGEYFFSDGIRLKKYRGM GSLDAM 420  
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Db 361 VIADGGI QNVGHI AKALALGASTVMMG SLLAATTEAPGEYFFSDGIRLKKYRGM GSLDAM 420  
  
Qy 421 DKHLSSQ NRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQD IGA KSLTQVR 480  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 421 DKHLSSQ NRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQD IGA KSLTQVR 480  
  
Qy 481 AMMYS GELKFEKRTSSAQVEGGVHSLHSYEKRLF 514  
||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 481 AMMYS GELKFEKRTSSAQVEGGVHSLHSYEKRLF 514

Database :           UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
<hr/>						
1	2595	99.1	514	1	IMD2_HUMAN	P12268 homo sapien
2	2561	97.8	514	1	IMD2_MOUSE	P24547 mus musculu
3	2559	97.7	514	1	IMD2_CRIGR	P12269 cricetus
4	2547	97.3	514	2	Q6P9U9	Q6p9u9 rattus norv
5	2422	92.5	514	2	Q66JD5	Q66jd5 xenopus tro
6	2411	92.1	514	2	Q7ZYP7	Q7zyp7 xenopus lae
7	2404	91.8	514	2	Q7ZXT8	Q7zxt8 xenopus lae
8	2395	91.4	514	2	Q7ZYW9	Q7zyw9 brachydanio
9	2256	86.1	514	2	Q7ZWN1	Q7zwn1 xenopus lae
10	2253	86.0	544	2	Q6GMG5	Q6gmg5 brachydanio
11	2234	85.3	514	1	IMD1_HUMAN	P20839 homo sapien
12	2222	84.8	514	2	Q7TSG7	Q7tsg7 mus musculu
13	2203	84.1	514	1	IMD1_MOUSE	P50096 mus musculu
14	2093.5	79.9	530	2	Q6ZNB1	Q6znb1 homo sapien
15	1830.5	69.9	559	2	Q7QHD0	Q7qhd0 anopheles g
16	1764.5	67.4	537	1	IMDH_DROME	Q07152 drosophila
17	1614.5	61.6	522	2	Q756Z6	Q756z6 ashbya goss
18	1610.5	61.5	524	1	IMD4 YEAST	P50094 saccharomyc
19	1608.5	61.4	526	2	Q6C897	Q6c897 yarrowia li
20	1607.5	61.4	523	1	IMD3 YEAST	P50095 saccharomyc
21	1605.5	61.3	521	1	IMH3_CANAL	O00086 candida alb
22	1597.5	61.0	521	2	Q9P8J2	Q9p8j2 candida alb